

241 SAKAVLTGKYKDELLESARGNEEKWALLTFLNVNCHASDGRKSTPLHLAAGYNRVKI 300  
301 VOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAAS 360  
301 VOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAAS 360  
301 VOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAAS 360  
361 KNRVEVCSLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEPKSHLSLQAAAREADVTR 420  
361 KNRVEVCSLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEPKSHLSLQAAAREADVTR 420  
421 IKKHLSEWVNFHPQTHETALHCAASAPYKPKOIICELLIRKGANINEKTEFLPLHV 480  
421 IKKHLSEWVNFHPQTHETALHCAASAPYKPKOIICELLIRKGANINEKTEFLPLHV 480  
481 ASEKANDVVEVVVKEAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQ 540  
481 ASEKANDVVEVVVKEAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQ 540  
541 FTALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVVKLCTVQSVNCRDIEGRQ 600  
541 FTALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVVKLCTVQSVNCRDIEGRQ 600  
601 STPLHFAAGYNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNM 660  
601 STPLHFAAGYNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNM 660  
661 VADLWFTPLHEAAKAGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQDLRGD 720  
661 VADLWFTPLHEAAKAGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQDLRGD 720  
721 AALLDAKKGCLARVKLSPPDNNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADV 780  
721 AALLDAKKGCLARVKLSPPDNNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADV 780  
781 AODKGLIPLHNAASGHVDVALLIKYNAACVNAWKWFTPLHEAAKAGRTOLCALLA 840  
781 AODKGLIPLHNAASGHVDVALLIKYNAACVNAWKWFTPLHEAAKAGRTOLCALLA 840  
841 HGAADPTLKQOEGTDLVSADVSALLTAAMPSPALPSYKQVNLGVRSFGATADALS 900  
841 HGAADPTLKQOEGTDLVSADVSALLTAAMPSPALPSYKQVNLGVRSFGATADALS 900  
901 SGSPSSLSAASSLNLSSGSELSSVSSSGTEGASSLEKKEKVPDVSITQFVRNLG 960  
901 SGSPSSLSAASSLNLSSGSELSSVSSSGTEGASSLEKKEKVPDVSITQFVRNLG 960  
961 LEHMDIFEREQITDLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPVLT 1020  
961 LEHMDIFEREQITDLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPVLT 1020  
1021 NTSGSGTILDLSPDKKEFOSVEEEMOSTVREHRDGHAGGIENRNVNLIKIQVCNKKLW 1080  
1021 NTSGSGTILDLSPDKKEFOSVEEEMOSTVREHRDGHAGGIENRNVNLIKIQVCNKKLW 1080  
1081 ERYTHRRKEVSEENHNANERMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSS 1140  
1081 ERYTHRRKEVSEENHNANERMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSS 1140  
1141 KSNQYVYGCGGCPVHKDRSCVICHROLFCRVTLGKSFLOFSAMKMAHSPGHHSVT 1200  
1141 KSNQYVYGCGGCPVHKDRSCVICHROLFCRVTLGKSFLOFSAMKMAHSPGHHSVT 1200  
1201 GRPSVNGLALAEVYVIRGEQAYPEYLITYQIMRPEGMDVG 1240  
1201 GRPSVNGLALAEVYVIRGEQAYPEYLITYQIMRPEGMDVG 1240

RESULT 2  
US-10-199-937-107  
Sequence 107, Application US/10199937  
Publication No. US20030190739A1  
EXPIRATION INFORMATION:  
APPLICANT: Christenson, Erik

BEST AVAILABLE COPY

APPLICANT: DeMaggio, Anthony J.  
APPLICANT: Goldman, Phyllis S.  
APPLICANT: McElligott, David L.  
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS  
FILE REFERENCE: 27866/36559  
CURRENT APPLICATION NUMBER: US/10/199,937  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US/09/606,035  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/141,582  
PRIOR FILING DATE: 1999-06-29  
NUMBER OF SEQ ID NOS: 178  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 107  
LENGTH: 1262  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-199-937-107

Query Match 98.6%; Score 6375.5; DB 4; Length 1262;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 6 RGAGCGGAGRGARVGAHGTAPDPTAGSQAARALSASSPGGLALLLAGPGLLLALL 65  
DB 29 RGRSGAGSPARGAR-GRGHTAPDPTAGSQAARALSASSPGGLALLLAGPGLLLALL 87  
QY 66 LLAVALAARIMSGRCAGGGAACASAAAEEAVEPAARELFEACRNGDVVERKRLVTPKVN 125  
DB 88 LLAVALAARIMSGRCAGGGAACASAAAEEAVEPAARELFEACRNGDVVERKRLVTPKVN 147  
QY 126 RTAGRKSTPLHFAAGFGKDVVYLLQNGANVQARDGGLIPLHNACSFHAEVNNLL 185  
DB 148 RTAGRKSTPLHFAAGFGKDVVYLLQNGANVQARDGGLIPLHNACSFHAEVNNLL 207  
QY 186 RGAADPNARDNNYTPLEAAIKGKIDVICVILQHGAEPTIRNTDGTALDADPSAKAV 245  
DB 208 RHGADPNARDNNYTPLEAAIKGKIDVICVILQHGAEPTIRNTDGTALDADPSAKAV 267  
QY 246 LTGEYKDELLESARGNEEKWALLTFLNVNCHASDGRKSTPLHLAAGYNRVKI 305  
DB 268 LTGEYKDELLESARGNEEKWALLTFLNVNCHASDGRKSTPLHLAAGYNRVKI 327  
QY 306 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAASKNRVE 365  
DB 328 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAASKNRVE 387  
QY 366 VCSLLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEPKSHLSLQAAAREADVTRIK 425  
DB 388 VCSLLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEPKSHLSLQAAAREADVTRIK 447  
QY 426 SLEWVNFHPQTHETALHCAASAPYKPKOIICELLIRKGANINEKTEFLPLHVASEKA 485  
DB 448 SLEWVNFHPQTHETALHCAASAPYKPKOIICELLIRKGANINEKTEFLPLHVASEKA 507  
QY 486 HNDVVEVVVKEAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGTALQ 545  
DB 508 HNDVVEVVVKEAKVNDLNGOTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGTALQ 567  
QY 546 MGNENVQQLQEGISLGNSEADROLLEAAKAGDVETVVKLCTVQSVNCRDIEGRQSTPLH 605  
DB 568 MGNENVQQLQEGISLGNSEADROLLEAAKAGDVETVVKLCTVQSVNCRDIEGRQSTPLH 627  
QY 606 FAAGYNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLM 665  
DB 628 FAAGYNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLM 687  
QY 666 KFTPLHEAAKAGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQDLRGDAALLD 725  
DB 688 KFTPLHEAAKAGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQDLRGDAALLD 747  
QY 726 AAKKGLARVKLSPPDNNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKG 785

Db 748 AAKGCLARVKKLSPPDNVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 807  
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHEAAOKGRTQLCALLAHGADP 845  
Db 808 GLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHEAAOKGRTQLCALLAHGADP 867  
Qy 846 TLKNOEGQTPDLVSADDSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGPSS 905  
Db 868 TLKNOEGQTPDLVSADDSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGPSS 927  
Qy 906 PSSLSAASLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLM 965  
Db 928 PSSLSAASLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLM 987  
Qy 966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGS 1025  
Db 988 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGS 1047  
Qy 1026 GTILDLSPDDKKEFOSVEEEMQSTVREHRDGGHAGGIFRNYNLKTKQVCKNKKLWERYTH 1085  
Db 1048 GTILDLSPDDKKEFOSVEEEMQSTVREHRDGGHAGGIFRNYNLKTKQVCKNKKLWERYTH 1107  
Qy 1086 RRKEVESEENHNHNERMLPHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQY 1145  
Db 1108 RRKEVESEENHNHNERMLPHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQY 1167  
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMQMAHSPPGHHSVTGRPSV 1205  
Db 1168 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMQMAHSPPGHHSVTGRPSV 1227  
Qy 1206 NGLALAEYVIRGEQAYPEYLITYQIMRPEGVMDG 1240  
Db 1228 NGLALAEYVIRGEQAYPEYLITYQIMRPEGVMDG 1262

## RESULT 3

US-10-199-937-133  
; Sequence 133, Application US/10199937  
; Publication No. US20030190749A1  
; GENERAL INFORMATION:  
; APPLICANT: Christenson, Erik  
; APPLICANT: DeMaggio, Anthony J.  
; APPLICANT: Goldman, Phyllis S.  
; APPLICANT: McElligott, David L.  
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS  
; FILE REFERENCE: 27866/36559  
; CURRENT APPLICATION NUMBER: US/10/199,937  
; PRIORITY FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/606,035  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/141,582  
; PRIOR FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 178  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 133  
; LENGTH: 1385  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-199-937-133

Query Match 98.8%; Score 6375.5; DB 4; Length 1385;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;  
Qy 6 RGAAGGCGAQRGARVGAHCTAPDPVTAGSOAARALSSAPGGLALLAGPGLLELLAL 65  
Db 152 RGRGAGSPARGAR-GRGHGTAPDPVTAGSOAARALSSAPGGLALLAGPGLLELLAL 210  
Qy 66 LLAAVAARIMSGRCAGGGAACAASAAAEVPAARELFEACRNGDVERVKRLVTPPEKNS 125  
Db 211 LLAAVAARIMSGRCAGGGAACAASAAAEVPAARELFEACRNGDVERVKRLVTPPEKNS 270  
Qy 126 RTAGRKSTPLHFAAGFGKRDVVEYLLQNGANVQARDDGGLIPLHNACSGHAEVNVNLLL 185

Db 271 RTAGRKSTPLHFAAGFGKRDVVEYLLQNGANVQARDDGGLIPLHNACSGHAEVNVNLLL 330  
Qy 186 RHGADPNARDNNWYTPLEHAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAV 245  
Db 331 RHGADPNARDNNWYTPLEHAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAV 390  
Qy 246 LTGEYKKBELLSESARGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIQVOLL 305  
Db 391 LTGEYKKBELLSESARGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIQVOLL 450  
Qy 306 QHGADVHAOKGDLVPLHNACSYGHVEVTELVKHCACVNMADLWQFTPLHEAASKRVE 365  
Db 451 QHGADVHAOKGDLVPLHNACSYGHVEVTELVKHCACVNMADLWQFTPLHEAASKRVE 510  
Qy 366 VCSLLSYGADPTLNLCHNKSALDAPTPOLKERLAYEPKSHSLLQAAREADVTRIKKHL 425  
Db 511 VCSLLSYGADPTLNLCHNKSALDAPTPOLKERLAYEPKSHSLLQAAREADVTRIKKHL 570  
Qy 426 SLEWVNFKIPOTHETALHCAAAASPPYKQKICELLRLKGANINEKTEFELTPLHVAASEKA 485  
Db 571 SLEWVNFKIPOTHETALHCAAAASPPYKQKICELLRLKGANINEKTEFELTPLHVAASEKA 630  
Qy 486 HNDVVEVVKHEAKYNALDNLGOTSILHRAAYCGHLOTCELLLSYGCDDPNTISI-OGFTALQ 545  
Db 631 HNDVVEVVKHEAKYNALDNLGOTSILHRAAYCGHLOTCELLLSYGCDDPNTISI-OGFTALQ 690  
Qy 546 MGENVQQLQSGISIGNSEADRLLEAAKAGDVETVKKLCVTVQSVNCRDIEGRQSTPLH 605  
Db 691 MGENVQQLQSGISIGNSEADRLLEAAKAGDVETVKKLCVTVQSVNCRDIEGRQSTPLH 750  
Qy 606 PAAGYNNRVSVVEYLLQHGADVHAOKGGLVPLHNACSYGHVEVTELVKHCACVNMADLW 665  
Db 751 PAAGYNNRVSVVEYLLQHGADVHAOKGGLVPLHNACSYGHVEVTELVKHCACVNMADLW 810  
Qy 666 KFTPLHEAAAKGKYEICKLLOHGADPTKKNRDNTPDLVKDGDTDIOQLLRGDAALLD 725  
Db 811 KFTPLHEAAAKGKYEICKLLOHGADPTKKNRDNTPDLVKDGDTDIOQLLRGDAALLD 870  
Qy 726 AAKGCLARVKKLSPPDNVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785  
Db 871 AAKGCLARVKKLSPPDNVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 930  
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHEAAOKGRTQLCALLAHGADP 845  
Db 931 GLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHEAAOKGRTQLCALLAHGADP 990  
Qy 846 TLKNOEGQTPDLVSADDSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGPSS 905  
Db 991 TLKNOEGQTPDLVSADDSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGPSS 1050  
Qy 906 PSSLSAASLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLM 965  
Db 1051 PSSLSAASLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLM 1110  
Qy 966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGS 1025  
Db 1111 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGS 1170  
Qy 1026 GTILDLSPDDKKEFOSVEEEMQSTVREHRDGGHAGGIFRNYNLKTKQVCKNKKLWERYTH 1085  
Db 1171 GTILDLSPDDKKEFOSVEEEMQSTVREHRDGGHAGGIFRNYNLKTKQVCKNKKLWERYTH 1230  
Qy 1086 RRKEVESEENHNHNERMLPHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQY 1145  
Db 1231 RRKEVESEENHNHNERMLPHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQY 1290  
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMQMAHSPPGHHSVTGRPSV 1205  
Db 1291 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMQMAHSPPGHHSVTGRPSV 1350  
Qy 1206 NGLALAEYVIRGEQAYPEYLITYQIMRPEGVMDG 1240

Db	727	VAALLIKYNACVNTDKWAFPLHEAAQKGRTOCALLAHGADPTLKNQEGOTPLDLVS	786
Qy	721	ADVSALLTAAMPSPALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLSS	780
Db	787	ADVSALLTAAMPSPALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLSS	846
Qy	781	SFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLTLVVE	840
Db	847	SFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLTLVVE	906
Qy	841	MGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPYLTLNTSGSTLILDLSPDDKEFQ	900
Db	907	MGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPYLTLNTSGSTLILDLSPDDKEFQ	966
Qy	901	SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENHNHANE	960
Db	967	SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENHNHANE	1026
Qy	961	RMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGCGTGPCVHKD	1020
Db	1027	RMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGCGTGPCVHKD	1086
Qy	1021	RSYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV	1065
Db	1087	RSYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV	1131
RESULT 6			
US-10-199-937-135			
; Sequence 135, Application US/10199937			
; Publication No. US20030190739A1			
; GENERAL INFORMATION:			
; APPLICANT: Christenson, Erik			
; APPLICANT: DeMaggio, Anthony J.			
; APPLICANT: Goldman, Phyllis S.			
; APPLICANT: McElligott, David L.			
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS			
; FILE REFERENCE: 27866/36559			
; CURRENT APPLICATION NUMBER: US/10/199,937			
; CURRENT FILING DATE: 2002-07-22			
; PRIOR APPLICATION NUMBER: US/09/606,035			
; PRIOR FILING DATE: 2000-06-28			
; PRIOR APPLICATION NUMBER: 60/141,582			
; PRIOR FILING DATE: 1999-06-29			
; NUMBER OF SEQ ID NOS: 178			
; SOFTWARE: Patent in Ver. 2.0			
; SEQ ID NO 135			
; LENGTH: 1166			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-199-937-135			
Query Match 99.9%; Score 5582; DB 4; Length 1166;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GFGKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVYNLLLRHGADPNARDNNYT	60
Db	67	GFGKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVYNLLLRHGADPNARDNNYT	126
Qy	61	PLHEAAIKGIDVCIVLQHGAEPTIRNTDRTALDADPSAKAVLTGEYKDELESAR	120
Db	127	PLHEAAIKGIDVCIVLQHGAEPTIRNTDRTALDADPSAKAVLTGEYKDELESAR	186
Qy	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLV	180
Db	187	SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLV	246
Qy	181	PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAKRNVEVCSLLSLLSGADPTLL	240
Db	247	PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAKRNVEVCSLLSLLSGADPTLL	306

Qy	241	NCHNKAIDLAPTPOKERLAYEFKHSLLQAREADVTIRIKKHSLEWVNFKHPQTHET	300
Db	307	NCHNKAIDLAPTPOKERLAYEFKHSLLQAREADVTIRIKKHSLEWVNFKHPQTHET	366
Qy	301	ALHCAAAAPYPRKQICELLERKGANINEKTEFTPLHVASEKAHNDVVEVVVHEAKV	360
Db	367	ALHCAAAAPYPRKQICELLERKGANINEKTEFTPLHVASEKAHNDVVEVVVHEAKV	426
Qy	361	NALDNLGOTSLEHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQMGNEVQQLLQEGIS	420
Db	427	NALDNLGOTSLEHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQMGNEVQQLLQEGIS	486
Qy	421	LGNSEADROLLEAAKAGDVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLL	480
Db	487	LGNSEADROLLEAAKAGDVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLL	546
Qy	481	QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVVNVADLWKFPLHEAAAGKYE	540
Db	547	QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVVNVADLWKFPLHEAAAGKYE	606
Qy	541	ICKLLLOHGADPTKKNRDGNTPLDVLKDGDDTDIQLLRGDAALLDAACKGCLARVKLSS	600
Db	607	ICKLLLOHGADPTKKNRDGNTPLDVLKDGDDTDIQLLRGDAALLDAACKGCLARVKLSS	666
Qy	601	PONVNCRTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD	660
Db	667	PONVNCRTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD	726
Qy	661	VAALLIKYNACVNTDKWAFPLHEAAQKGRTOCALLAHGADPTLKNQEGOTPLDLVS	720
Db	727	VAALLIKYNACVNTDKWAFPLHEAAQKGRTOCALLAHGADPTLKNQEGOTPLDLVS	786
Qy	721	ADVSALLTAAMPSPALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLSS	780
Db	787	ADVSALLTAAMPSPALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLSS	846
Qy	781	SFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLTLVVE	840
Db	847	SFSELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLTLVVE	906
Qy	841	MGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPYLTLNTSGSTLILDLSPDDKEFQ	900
Db	907	MGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPYLTLNTSGSTLILDLSPDDKEFQ	966
Qy	901	SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENHNHANE	960
Db	967	SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENHNHANE	1026
Qy	961	RMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGCGTGPCVHKD	1020
Db	1027	RMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGCGTGPCVHKD	1086
Qy	1021	RSYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV	1065
Db	1087	RSYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV	1131
RESULT 7			
US-10-199-937-2			
; Sequence 2, Application US/10199937			
; Publication No. US20030190739A1			
; GENERAL INFORMATION:			
; APPLICANT: Christenson, Erik			
; APPLICANT: DeMaggio, Anthony J.			
; APPLICANT: Goldman, Phyllis S.			
; APPLICANT: McElligott, David L.			
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS			
; FILE REFERENCE: 27866/36559			
; CURRENT APPLICATION NUMBER: US/10/199,937			
; CURRENT FILING DATE: 2002-07-22			
; PRIOR APPLICATION NUMBER: US/09/606,035			
; PRIOR FILING DATE: 2000-06-28			
; PRIOR APPLICATION NUMBER: 60/141,582			
; PRIOR FILING DATE: 1999-06-29			
; NUMBER OF SEQ ID NOS: 178			
; SOFTWARE: Patent in Ver. 2.0			
; SEQ ID NO 135			
; LENGTH: 1166			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-199-937-135			

Db 781 SFSELSVSSVSSGTSAGSLEKEVGVDPSTQTFVNLGLEHLMDFPERQITLDVLVE 840  
Qy 841 MGHEKEIGINAYGHRHKLKGVVRLISGOQGLNPLYTLNTSGSTILIDLSPPDKPEQ 900  
Db 841 MGHEKEIGINAYGHRHKLKGVVRLISGOQGLNPLYTLNTSGSTILIDLSPPDKPEQ 900  
Qy 901 SYVEEMQSTVREHROGCHAGGIFNRNIIKIOKVCNKKLWERYTHRRKEVSENNHANE 960  
Db 901 SYVEEMQSTVREHROGCHAGGIFNRNIIKIOKVCNKKLWERYTHRRKEVSENNHANE 960  
Qy 961 RMLFHGSPFNALIIHKGDFDERHAYIIGMFGAGIYFAENSCKSNQYVYGIGGTGCPVHKD 1020  
Db 961 RMLFHGSPFNALIIHKGDFDERHAYIIGMFGAGIYFAENSCKSNQYVYGIGGTGCPVHKD 1020  
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1065  
Db 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1065  
RESULT 13  
US-09-509-196A-2  
Sequence 2, Application US/09509196A  
Patent No. US20020037582A1  
GENERAL INFORMATION:  
; APPLICANT: DALY, Roger J.  
; APPLICANT: SUTHERLAND, Robert L.  
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: 1871-129  
; CURRENT APPLICATION NUMBER: US/09/509,196A  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: P09388  
; PRIOR FILING DATE: 1997-09-23  
; PRIOR APPLICATION NUMBER: PCT AU98/00795  
; PRIOR FILING DATE: 1998-09-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1074  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-509-196A-2  
Query Match 97.1%; Score 5421; DB 3; Length 1074;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1034; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 27 IPLHNACSFHAEVNNLLRHGADPNARDNWNVTPLHEAAIKGKIDVICIVLLQHGAEPTI 86  
Db 1 IPLHNACSFHAEVNNLLRHGADPNARDNWNVTPLHEAAIKGKIDVICIVLLQHGAEPTI 60  
Qy 87 RNTDGRDALDAPSAKAVLTGEYKDDLESARSNGNEEKWALLTPLNVNCHASDGRKS 146  
Db 61 RNTDGRDALDAPSAKAVLTGEYKDDLESARSNGNEEKWALLTPLNVNCHASDGRKS 120  
Qy 147 TPLHLAGYNNRKYVQLLQHGADVHAKDGLVPLHNACSYGHHYVTELLVKGACVNA 206  
Db 121 TPLHLAGYNNRKYVQLLQHGADVHAKDGLVPLHNACSYGHHYVTELLVKGACVNA 180  
Qy 207 MDLWQFTPLHEAASKNEVEVCSLLSYGADPTLNCNKSALDIAPTPOLKERLAYEFKG 266  
Db 181 MDLWQFTPLHEAASKNEVEVCSLLSYGADPTLNCNKSALDIAPTPOLKERLAYEFKG 240  
Qy 267 HSLLOAAREADVTRIKKHSLEWVNFKHPOTHETALHCAASPYKQICELLRRKAN 326  
Db 241 HSLLOAAREADVTRIKKHSLEWVNFKHPOTHETALHCAASPYKQICELLRRKAN 300  
Qy 327 INEKTKEFLTPHVAASEKANDVVEVVVHKAQNALDNLGQTSILHRAAYGHLQTCRLL 386  
Db 301 INEKTKEFLTPHVAASEKANDVVEVVVHKAQNALDNLGQTSILHRAAYGHLQTCRLL 360  
387 LSYGCDPNIISLOQFTALQMGNEVQQLQSGISGNSEADROLLEAAKAGDVETVKKLC 446

Db 361 LSYGCDPNIISLOQFTALQMGNEVQQLQSGISGNSEADROLLEAAKAGDVETVKKLC 420  
Qy 447 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQHGADVHAKDGLVPLHNACSYGHHY 506  
Db 421 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYLLQHGADVHAKDGLVPLHNACSYGHHY 480  
Qy 507 EVAELLVKGAVNVVADLWKFTPLHEAAAKKYEICKLLLOHGADPTKKNRDNTPDLV 566  
Db 481 EVAELLVKGAVNVVADLWKFTPLHEAAAKKYEICKLLLOHGADPTKKNRDNTPDLV 540  
Qy 567 KQDPTDIQDLARGDAALDAKKGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNL 626  
Db 541 KQDPTDIQDLARGDAALDAKKGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNL 600  
Qy 627 EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAATDKWFTPLHEA 686  
Db 601 EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNASLNATDKWFTPLHEA 660  
Qy 687 AQKGTQLCALLAHGADPTLKNQEGQTPDLVSADDDVSALLTAAMPPSALPSCYKQVIL 746  
Db 661 AQKGTQLCALLAHGADPTLKNQEGQTPDLVSADDDVSALLTAAMPPSALPSCYKQVIL 720  
Qy 747 NGVRSFGATADALSGSPSSLSAASLDNLSSGSELSVSSVSSGTEGASSLEKKEVP 806  
Db 721 NGVRSFGATADALSGSPSSLSAASLDNLSSGSELSVSSVSSGTEGASSLEKKEVP 780  
Qy 807 GYDPSITQFVRLNGLEHLMDFPERQITLDVLVENGHEKELKEIGINAYGHRHKLKGVVER 866  
Db 781 GYDPSITQFVRLNGLEHLMDFPERQITLDVLVENGHEKELKEIGINAYGHRHKLKGVVER 840  
Qy 867 LISGOQGLNPLYTLNTSGSTILIDLSPPDKKEFQSVVEEMQSTVREHROGCHAGGIFNRY 926  
Db 841 LISGOQGLNPLYTLNTSGSTILIDLSPPDKKEFQSVVEEMQSTVREHROGCHAGGIFNRY 900  
Qy 927 NILKIQKVCNKKLWERYTHRRKEVSENNHANEHMLPHGSPFNALIIHKGDFDERHAYIG 986  
Db 901 NILKIQKVCNKKLWERYTHRRKEVSENNHANEHMLPHGSPFNALIIHKGDFDERHAYIG 960  
Qy 987 GMFGAGIYFAENSCKSNQYVYGIGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSA 1046  
Db 961 GMFGAGIYFAENSCKSNQYVYGIGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOFSA 1020  
Qy 1047 MKWAHSPGHHSVTGRPSV 1065  
Db 1021 MKWAHSPGHHSVTGRPSV 1039  
RESULT 14  
US-09-849-602-26  
Sequence 26, Application US/09849602  
Publication No. US20030165834A1  
GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew J.  
; APPLICANT: Old, Lloyd J.  
; APPLICANT: Stockert, Elisabeth  
; APPLICANT: Chen, Yao-Tseung  
; TITLE OF INVENTION: Colon Cancer Antigen Panel  
; FILE REFERENCE: L0461/7105 (JRV)  
; CURRENT APPLICATION NUMBER: US/09/849,602  
; CURRENT FILING DATE: 2001-05-04  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-849-602-26  
Query Match 96.0%; Score 5363.5; DB 3; Length 1227;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 1035; Conservative 3; Mismatches 25; Indels 3; Gaps 2;

	Query Match	99.9%;	Score 5582;	DB 2;	Length 1166;
	Best Local Similarity	99.9%;	Pred. No. 0;		
	Matches 1064;	Conservative	1;	Mismatches	0; Indels
					0; Gaps
QY	1	GFGKDVVEYLLONGASVQARDGGGLIPLHNACSFHGAEEVNNLLRHGDADPNARDNNWNT	60		
DB	67	GFGKDVVEYLLONGAVQARDGGGLIPLHNACSFHGAEEVNNLLRHGDADPNARDNNWNT	126		
QY	61	PLPHEAAIKGIDVCTVLLHQHGAEPTRNTDGRALTDLADPSAKAVLTGYKKDLELSAR	120		

Db 127 PLHEAAIKGKIDVCIVLQHGAEPIRTNDGRTALDADPSAKAVLTGEYKDELLESAR 186  
Qy 121 SGNEKMWALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180  
Db 187 SGNEKMWALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 246  
Qy 181 PLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHFAASKNRVEVCSLLSYGADPTLL 240  
Db 247 PLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHFAASKNRVEVCSLLSYGADPTLL 306  
Qy 241 NCHNKAIDLAPTQKRLAYEFKHSLLQAREADVTRIKKHLSENVNFKPQTHET 300  
Db 307 NCHNKAIDLAPTQKRLAYEFKHSLLQAREADVTRIKKHLSENVNFKPQTHET 366  
Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFTPLHFAASEKANDVVEVVKHEAKV 360  
Db 367 ALHCAASPYPKRKQICELLRKGANINEKTEFTPLHFAASEKANDVVEVVKHEAKV 426  
Qy 361 NALDNLGOTSILHRAAYCGHLOTCLLLSYGCDPNIIISLGFTALQMGNEVQOQLQEGIS 420  
Db 427 NALDNLGOTSILHRAAYCGHLOTCLLLSYGCDPNIIISLGFTALQMGNEVQOQLQEGIS 486  
Qy 421 LGNEADRLQLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480  
Db 487 LGNEADRLQLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 546  
Qy 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHFAASEKANDVVEVVKHEAKV 540  
Db 547 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCACVNMADLWQFTPLHFAASEKANDVVEVVKHEAKV 606  
Qy 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTHDIQDLRGDAALLDAAKGGCLARVKLSS 600  
Db 607 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTHDIQDLRGDAALLDAAKGGCLARVKLSS 666  
Qy 601 PDNVNCRDTQGRHSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 660  
Db 667 PDNVNCRDTQGRHSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 726  
Qy 661 VAALLIKYNACVNAATDKWAFPLHFAAGYNNRVKIVOLLQHGADVHAKDGLV 720  
Db 727 VAALLIKYNACVNAATDKWAFPLHFAAGYNNRVKIVOLLQHGADVHAKDGLV 786  
Qy 721 ADDVSALLTAAMPSPSALPSYKPOVLNGVRSFGATADALSSGSPSSLSAASSLDNLSS 780  
Db 787 ADDVSALLTAAMPSPSALPSYKPOVLNGVRSFGATADALSSGSPSSLSAASSLDNLSS 846  
Qy 781 SPSELSSVSSSGTSGASLEKKEVPGVDFSTIQFVRNLGLHMDIPEREQITLDVLVE 840  
Db 847 SPSELSSVSSSGTSGASLEKKEVPGVDFSTIQFVRNLGLHMDIPEREQITLDVLVE 906  
Qy 841 MGHKELKEIGINAYGHRHKLKGVRELISGQGLNPLYLTNTSGSTILIDLSPDKBFQ 900  
Db 907 MGHKELKEIGINAYGHRHKLKGVRELISGQGLNPLYLTNTSGSTILIDLSPDKBFQ 966  
Qy 901 SVEEMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHANE 960  
Db 967 SVEEMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHANE 1026  
Qy 961 RMLFHGSPFNVAI IHKGFDERHAYIGMFGAGIYFAENSKSNQVYVYGGTGCPVHKD 1020  
Db 1027 RMLFHGSPFNVAI IHKGFDERHAYIGMFGAGIYFAENSKSNQVYVYGGTGCPVHKD 1086  
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065  
Db 1087 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1131

RESULT 5

US-09-696-668-4

Sequence 4, Application US/0969668

Patent No. 6617102

GENERAL INFORMATION:

541 ICKLLQHGADPKKRDGNTPLDLVKGDTDIHYLLRGDAALLDAKKGCLARVKLSS 600  
 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660  
 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660  
 661 VAALLIKYNACVNATDKWAFPLHAAQKGTQOLCALLAHAGADPTLKNQEGTPLDLVS 720  
 661 VAALLIKYNACVNATDKWAFPLHAAQKGTQOLCALLAHAGADPTLKNQEGTPLDLVS 720  
 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLG 780  
 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLG 780  
 781 SFSELSSVSSSGTEGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840  
 781 SFSELSSVSSSGTEGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840  
 841 MGHEKELKEIGINAYGHRHKLKIGVERLISQOGLNPLYTLNTSGSGTILIDSPDDKEFO 900  
 841 MGHEKELKEIGINAYGHRHKLKIGVERLISQOGLNPLYTLNTSGSGTILIDSPDDKEFO 900  
 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960  
 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960  
 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGTGCPCVHKD 1020  
 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGTGCPCVHKD 1020  
 1021 RSCYICHRQLLFCRVTLGKSFQFSAMKVAHSPPGHHSVTGRPSV 1065  
 1021 -SCYICHRQLLFCRVTLGKSFQFSAMKVAHSPPGHHSVTGRPSV 1064

RESULT 9  
 US-09-350-982C-5  
 Sequence 5, Application US/09350982C  
 Patent No. 6455290  
 GENERAL INFORMATION:  
 APPLICANT: Berthelsen, Jens  
 APPLICANT: Toma, Salvatore  
 APPLICANT: Isacchi, Antonella  
 TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Rel  
 TITLE OF INVENTION: Same  
 FILE REFERENCE: PHRM-0043  
 CURRENT APPLICATION NUMBER: US/09/350,982C  
 CURRENT FILING DATE: 1999-07-09  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5  
 LENGTH: 1166  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: Xaa is any amino acid  
 NAME/KEY: misc feature  
 LOCATION: (1102)..(1102)  
 OTHER INFORMATION: n is any nucleic acid  
 NAME/KEY: misc feature  
 LOCATION: (2650)..(2650)  
 OTHER INFORMATION: n is any nucleic acid  
 US-09-350-982C-5

Query Match 99.1%; Score 5533; DB 2; Length 1166;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1056; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 1 GGRKDVVEYLLONGASVQARDGGGLIPLHNAACFHAIEVNNLLRHGADPNARDNNYT 60  
 67 GGRKDVVEYLLONGASVQARDGGGLIPLHNAACFHAIEVNNLLRHGADPNARDNNYT 126

61 PLHEAAIKGIDVICIVLLQHGABPTIRNTDGTALDADPSAKAVLTGEYKODELLESAR 120  
 127 PLHEAAIKGIDVICIVLLQHGABPTIRNTDGTALDADPSAKAVLTGEYKODELLESAR 186  
 121 SGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVNAQDKGLV 180  
 187 SGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVNAQDKGLV 246  
 181 PLHNACSYGHEVTELLVKGACVNAMDQWQFTPLHEAASKNRVEVCSSLISYGDPTLL 240  
 247 PLHNACSYGHEVTELLVKGACVNAMDQWQFTPLHEAASKNRVEVCSSLISYGDPTLL 306  
 241 NCHNKAIDLAPTPOLKERLAYEFKSHLSLQAAAREADVTRI KKHLSLEWNVFKHPQTHET 300  
 307 NCHNKAIDLAPTPOLKERLAYEFKSHLSLQAAAREADVTRI KKHLSLEWNVFKHPQTHET 366  
 301 ALHCAASPYPRKQICELLIRKGANINEKTEFETPLHVAASEKAHNDVVEVVVHEAKV 360  
 367 AXHCAASPYPRKQICELLIRKGANINEKTEFETPLHVAASEKAHNDVVEVVVHEAKV 426  
 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQMGNNVQOLLQEGIS 420  
 427 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQMGNNVQOLLQEGIS 486  
 421 LGNSEADRLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480  
 487 LGNSEADRLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 546  
 481 QHGADVNAQDKGGLIPLHNAACSYGHEVVAELLVKGACVNAMDQWQFTPLHFAAAGKGYE 540  
 547 QHGADVNAQDKGGLIPLHNAACSYGHEVVAELLVKGACVNAMDQWQFTPLHFAAAGKGYE 606  
 541 ICKLLQHGADPKKRDGNTPLDLVKGDTDIQDLRGDAALLDAKKGCLARVKLSS 600  
 607 ICKLLQHGADPKKRDGNTPLDLVKGDTDIQDLRGDAALLDAKKGCLARVKLSS 666  
 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660  
 667 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726  
 661 VAALLIKYNACVNATDKWAFPLHAAQKGTQOLCALLAHAGADPTLKNQEGTPLDLVS 720  
 727 VAALLIKYNACVNATDKWAFPLHAAQKGTQOLCALLAHAGADPTLKNQEGTPLDLVS 786  
 721 ADDVSALLTAAMPSPSALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLG 780  
 787 ADDVSALLTAAMPSPSALPCYKQVINGVRSFGATADALSSGSPSSLSAASSLNLG 846  
 781 SFSELSSVSSSGTEGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840  
 847 SFSELSSVSSSGTEGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 906  
 841 MGHEKELKEIGINAYGHRHKLKIGVERLISQOGLNPLYTLNTSGSGTILIDSPDDKEFO 900  
 907 MGHEKELKEIGINAYGHRHKLKIGVERLISQOGLNPLYTLNTSGSGTILIDSPDDKEFO 966  
 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960  
 967 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 1026  
 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGTGCPCVHKD 1020  
 1027 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGTGCPCVHKD 1086  
 1021 RSCYICHRQLLFCRVTLGKSFQFSAMKVAHSPPGHHSVTGRPSV 1065  
 1087 RSCYICHRQLLFCRVTLGKSFQFSAMKVAHSPPGHHSVTGRPSV 1131

RESULT 10  
 US-09-849-602-26  
 ; Sequence 26, Application US/09849602



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